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DOUBLE MUTANTS OF DIHYDROFOLATE REDUCTASE AND METHODS OF USING SAME

DESCRIPTION

The invention described herein was made in the course of work under Grant No. CA-08010 from the National Institutes of Health. The United States government may have certain rights in this invention.

BACKGROUND OF THE INVENTION

5 This application relates to a new mutants of the enzyme dihydrofolate reductase, and to the use of these mutants as selectable markers and for gene therapy to produce drug resistant bone marrow or peripheral stem cells.

 Dihydrofolate reductase (DHFR, 5,6,7,8-tetrahydrofolate:NADP +
oxidoreductase, EC 1.5.1.3) catalyzes the NADPH-dependent reduction of dihydrofolate to
10 tetrahydrofolate, an essential carrier of one-carbon units in the biosynthesis of thymidylate,
purine nucleotides, serine and methyl compounds. DHFR is an essential enzyme in both
eukaryotes and prokaryotes.

 In rapidly dividing cells, the inhibition of DHFR results in the depletion of
cellular tetrahydrofolates, inhibition of DNA synthesis and cell death. Because of this, folate
15 analogs which inhibit DHFR, for example methotrexate (MTX), are used as antineoplastic
agents. The utility of "antifolate" treatments of this type is limited by two factors. First,
tumor tissues may rapidly develop resistance to the antifolate, rendering the treatment
ineffective. Second, the treatment may be toxic to rapidly dividing normal tissues, particularly
to bone marrow or peripheral stem cells.

20 International Patent Publication No. WO94/24277, which is incorporated
herein by reference, discloses mutant forms of human DHFR which have increased resistance
to inhibition by antifolates used in therapy including MTX. The specific mutants disclosed
differ from wild-type human DHFR as a result of a single mutation occurring at amino acid 15,
31 or 34.

25 Mutations at amino acid 22 of human DHFR have also been shown to reduce
the sensitivity of the enzyme to antifolate inhibition. Ercikan et al., in *Chemistry and Biology
of Pteridines and Folates*, J.E. Ayling, ed., Plenum Press (1993). In these mutants, the amino

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acids isoleucine, methionine, phenylalanine and tyrosine are substituted for the leucine of the wild-type enzyme.

SUMMARY OF THE INVENTION

5 The present invention provides new mutant forms of human DHFR which have properties superior to the previously disclosed mutants. In particular, the present application is addressed to mutant forms of human DHFR which have mutations at both amino acid 22 and amino acid 31. Preferred mutant forms within the scope of the invention are Ser31Tyr22, Ser31Phe22, Gly31Tyr22, Gly31Phe22, Ala31Tyr22 and Ala31Phe22.

10 The mutant DHFR of the invention may be used as a selectable marker. Thus, an aspect of the present invention is a method of selecting among clones for the introduction of a non-selectable gene comprising the steps of:

 (a) inserting the non-selectable gene into a DNA vector comprising DNA encoding a mutant form of human dihydrofolate reductase which differs from wild-type human
15 dihydrofolate reductase at both amino acid 22 and amino acid 31, wherein the mutant form has an amino acid with a larger volume side chain than leucine at amino acid 22 and an amino acid having a smaller volume, more hydrophilic side chain than phenylalanine at amino acid 31;

 (b) introducing the vector containing the non-selectable gene into cells of a type in which the non-selectable gene and the mutant form of dihydrofolate reductase are
20 expressed; and

 (c) selecting cells which are resistant to inhibition by antifolates.

 The mutant DHFR of the invention may also be used to modify the genome of human cells, particularly bone marrow cells or peripheral blood stem cells to render them resistant to chemotherapy using antifolate agents. Thus a further aspect of the invention is a
25 method for gene therapy comprising the steps of:

 (a) obtaining hematopoietic cells from a human patient;

 (b) transducing into the hematopoietic cells an expressible mutant form of human dihydrofolate reductase which differs from wild-type human dihydrofolate reductase at both amino acid 22 and amino acid 31, wherein the mutant form has an amino acid with a
30 larger volume side chain than leucine at amino acid 22 and an amino acid which having a smaller volume, more hydrophilic side chain than phenylalanine at amino acid 31; and

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(c) returning the transduced cells to the human patient.

BRIEF DESCRIPTION OF THE DRAWING

Fig. 1 shows a method as described by Higuchi et al. for introducing a specific mutation into a DNA sequence during PCR amplification.

DETAILED DESCRIPTION OF THE INVENTION

This application relates to "double-mutants" of human DHFR which differ from wild-type DHFR at both amino acid 22 and amino acid 31.

Wild-type DHFR has a leucine residue at amino acid 22 and a phenylalanine residue at amino acid 31. From studies of the crystal structure of DHFR, the leucine residue has been shown to be close to the active site and has been implicated in the formation of hydrophobic interactions with the folate enzyme substrate. In the mutants of the invention, the leucine residue is replaced with a residue which will disrupt binding of the mutant DHFR to antifolates. In particular, uncharged amino acid residues such as phenylalanine or tyrosine with larger side chains than leucine which will sterically hinder entry of the antifolate to the active site of the enzyme are suitable. Substitution of arginine at this position results in an inactive enzyme. Thus replacement with charged groups would appear to be unsuitable.

The normal phenylalanine residue at amino acid 31 has been shown to interact with the p-aminobenzoyl glutamate moiety of folate or antifolate substrates. Oefner et al., *Eur. J. Biochem* 174: 377-385 (1988). In the mutants of the invention, this phenylalanine is replaced with a small hydrophilic amino acid such as alanine, serine or glycine.

Mutant forms of human DHFR can be produced by site-directed mutagenesis of cDNA encoding wild-type human DHFR using the techniques described by Higuchi et al., *Nucleic Acids Res.* 16:7351-7367 (1988), which is incorporated herein by reference. In general, this procedure calls for the use of two sets of primers: a first pair which flanks the entire cDNA of DHFR and which therefore will produce a full length copy of the cDNA upon PCR amplification, and a second pair which are complementary to one another and which contain the desired mutation. These primers initially produce two sets of products, one having the mutation introduced near the 3'-end, and the other having the mutation introduced near the 5'-end. Because these two products are complementary to one another as well as to the PCR

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primers, however, the two products can form an overlapping duplex which is extended in both directions. Thus, PCR amplification of cDNA in the presence of these two primer sets results in full-length cDNA having the desired mutation as shown in Fig 1.

In the case of the double mutants of the invention, this procedure is performed twice. First, site-directed mutagenesis is performed to introduce a mutation at one of the two sites and to produce a single-mutant cDNA. This single-mutant cDNA is then subjected to the site-directed mutagenesis procedure a second time to introduce a mutation at the second site. The double-mutants of the invention can also be prepared by first preparing a Ser31 or Gly31 mutant as described in Schweitzer et al., *J. Biol. Chem.* 264: 20786-20795 (1989) and then introducing a mutation at amino acid 22 using the primers shown in Table 1 or primers complementary thereto.

TABLE 1 - PRIMERS FOR MUTATION AT AMINO ACID 22		
Introduced Amino Acid	Primer	
phenylalanine	5'-CCA GGG <u>TTT</u> GTC CCC GTT-3'	SEQ ID No. 1
tyrosine	5'-TGG CCA GGG <u>TAC</u> GTC CCC GTT CTT-3'	SEQ ID No. 2

Optimal mutants of DHFR for use in gene therapy applications will have two characteristics. First, the mutant should provide levels of DHFR activity with normal substrates which are sufficient to fulfill the function of uninhibited wild-type DHFR. Second, the mutant should continue to have this activity even in the presence of therapeutically effective levels of antifolates used in chemotherapy.

The extent to which a mutant form of DHFR has these characteristics can be preliminarily assessed by *in vitro* evaluation of several kinetic parameters, K_i , K_m , and k_{cat} . The first parameter, K_i , is the "inhibition constant" and reflects the level of inhibition by a given compound. K_i is obtained from steady state reaction rates observed for mixtures of enzyme, cofactor, 7,8-dihydrofolate (the normal substrate) and variable levels of antifolate. The higher the value of K_i , the higher the concentration of antifolate required to inhibit the activity of the enzyme on the normal substrate. Thus, preferred mutant enzymes for use in gene therapy applications will have values of K_i which are higher than those of wild-type DHFR.

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K_m or the "Michaelis constant" reflects the ability of an enzyme to convert a given substrate to product. In this case, the substrate is the normal substrate, 7,8-dihydrofolate. K_m is determined using a double reciprocal plot of the initial velocity of the reaction as a function of the concentration of the substrate. Higher values of K_m reflect a decreased affinity for the normal substrate. Thus, preferred mutant enzymes for use in gene therapy applications will have values of K_m which are as low as possible to be comparable to wild-type DHFR.

k_{cat} reflects the catalytic turnover of the enzyme. k_{cat} values are obtained by active site titration experiments using MTX or from activity and total protein measurements of purified enzyme species. Higher values of k_{cat} reflect a greater ability to convert substrate to product, and thus desirable mutant enzymes for use in gene therapy applications will have values of k_{cat} which are higher than those of wild-type DHFR.

The parameters K_m and k_{cat} can be combined to provide a measure of overall catalytic efficiency which is given by k_{cat}/K_m . High levels of catalytic efficiency are preferred. Further, the product of the catalytic efficiency and K_i provides an additional indicator of the properties of a mutant enzyme which takes into account the fact that lower levels of catalytic efficiency may be tolerable if the inhibitory effects of the inhibitor are sufficiently low.

Table 2 summarizes these kinetic parameters for several single mutations as well as for double mutations in accordance with the invention.

TABLE 2 - KINETIC PARAMETERS OF VARIANTS OF DHFR			
enzyme	K_m (H ₂ folate) (μ M)	k_{cat} (s ⁻¹)	k_{cat}/K_m (s ⁻¹ μ M ⁻¹)
wild type	0.08	12.7	159
31 serine	0.44	7.0	16
22 phenylalanine	0.16	7.4	46
22 tyrosine	0.15	1.5	10
31 serine 22 phenylalanine	0.44	1.6	3.6
31 serine 22 tyrosine	0.10	1.3	13

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Table 3 shows the interaction of these variants of DHFR with the antifolate methotrexate (MTX). As can be seen, the double mutants Ser31Phe22 and Ser31Tyr22 have K_i values which are much greater than those observed for the single mutants, as well as comparable catalytic efficiencies. These enzymes therefore have very high values for $K_i k_{cat}/K_m$ and are superior to the previously described single mutants for purposes of gene therapy to provide resistance to methotrexate toxicity.

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TABLE 3 CAPACITY OF VARIANTS TO CONFER MTX RESISTANCE				
enzyme	K_i (MTX)	k_{cat}/K_m ($s^{-1} \mu M^{-1}$)	$K_i \cdot K_{cat}/k_m$ (s^{-1})	relative
wt	1.2	159	0.191	1
F31S	239	16	3.82	20.0
L22F	106	46	4.88	25.5
L22Y	1980	10	19.8	104
F31S-L22F	25600	3.6	92.2	483
F31S-L22Y	12870	13	167	874

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Table 4 shows K_i values determined for the various forms of DHFR for several other antifolates, namely aminopterin (APT), trimetrexate (TMTX) and piritrexin (PTX). As in the case of methotrexate, the inhibition constant for the double mutants is much higher than that for the single mutants.

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TABLE 4 - BINDING OF ANTIFOLATES TO VARIANTS OF DHFR			
enzyme	K_i (pM)		
	APT	TMTX	PTX
wild type	1.8	13.0	13.2
31 serine	n.d.	n.d.	n.d.
22 phenylalanine	212	83.3	16.0
22 tyrosine	1277	2514	1190

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31 serine 22 phenylalanine	20600	19100	6370
31 serine 22 tyrosine	11740	116000	30300

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cDNA encoding mutant DHFR according to the invention can be introduced into hematopoietic stem cells via a retroviral vector to protect these cells from antifolate toxicity. Thus, a further aspect of the present invention is a retroviral vector which expresses a mutant human DHFR differing from wild-type human DHFR at both amino acids 22 and 31.

10 Such vectors are constructed by insertion of full length cDNA encoding the mutant human DHFR into a retrovirus such as Moloney murine leukemia virus-based N2 retroviral vector (MoMLV) modified to contain the SV40 early promoter, MoMLV modified to include the human β -actin promoter, an MFG-based vector which is a splicing vector without selectable marker that bears the MPSV 3'LTR or Gibbon Ape Leukemia Virus (GaLV) retroviral

15 particles with the GaLV envelope. The retroviral vector DNA is then packaged by transfection into a packaging cell line such as GP-E86 cells, an ecotropic packaging line or GP-AM12 cells or PG-13 cells, amphotropic packaging lines, for example by electroporation.

While amphotropic packaging for retroviral vectors has been widely used in hematopoietic gene transfer studies, the receptor for amphotropic viral particles, Ram-1, is

20 expressed at relatively low levels in hematopoietic cells. In contrast, the envelope of the GaLV binds to a receptor, called GLVR 1, which is highly expressed on this cell population. Therefore, one strategy which has been utilized to increase hematopoietic gene transfer efficiency has been to utilize a MoMLV based vector placed in a packaging cell line (called PG13) which produces viral particles with the GaLV envelope. Miller et al., *J. Virol.* 65:2220-2224 (1991). These particles should bind to hematopoietic cells (with their

25 increased GLVR 1 expression) with higher frequency and result in greater transduction efficiency. Riviere et al., *Proc. Nat'l Acad. Sci. (USA)* 92:6733-6737 (1995). Thus, a preferred approach to gene therapy using the mutant DHFR of the invention will make use of packaged retrovirus in PG13 or similar packaging cells which recognized and binds to the

30 GLVR1 receptor.

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The packaged retrovirus capable of expressing a mutant DHFR can be used to provide increased antifolate tolerance to patients undergoing antifolate therapy, thus permitting the usage of higher dosages of the antifolate chemotherapeutic agent. Peripheral blood stem cells (PBSC) are harvested by leukapheresis following treatment with G-CSF and optionally with chemotherapy (for example with cyclophosphamide). The CD34-positive population is selected for example with either a Cellpro Ceprate immunoaffinity column or immunomagnetic beads. The cells may be prestimulated for 72-96 hours in liquid culture in the presence of IL1, IL3, KL or Flk-2 Ligand. The CD34+ cells are infected by co-culture with the virus-producing cell line for 24 hours with cytokines (except IL1) and polybrene or protamine. After the infection, hematopoietic cells are expanded *in vitro* in suspension culture with weekly changes of media and growth factors. During this expansion, cells are exposed to the antifolate to be used in therapy to select for drug resistance.

Transduced PBSC CD34⁺ cells, optionally combined with untransduced CD34+ cells, are returned to the patient by transfusion following high dose chemotherapy. Beginning 24 hr. after transplant, the patient is treated with the antifolate. Relatively low, well-tolerated dosages may be used initially, with increasing dosages being given thereafter in the absence of indications of toxicity.

The use of transduced cells expressing mutant forms of DHFR to increase tolerance to antifolate drug therapy may be used for patients suffering from any type of cancer known to respond to the antifolate. The method of the invention is particularly suitable for use when the patient is suffering from breast cancer or advanced cancer of the head and neck.

In addition to use in gene therapy to provide hematopoietic cells with resistance to antifolate chemotherapeutic agents, the retroviral vectors of the invention may be used as selectable markers to facilitate the introduction of non-selectable genes into cells for therapeutic purposes. Variant forms of DHFR cDNAs are particularly attractive for this purpose, as they are relatively small and thus other genes can be accommodated in retroviral vectors.

EXAMPLE 1

Double-mutant DHFR enzymes in accordance with the invention were created by site-directed mutagenesis. Each of the mutations was introduced separately, using a polymerase chain reaction technique involving two separate sets of primers; one set flanking

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the entire cDNA of DHFR and the second set being complimentary to each other and containing the desired mutations.

In the first step, a serine residue was introduced at amino acid 31 as described in Schweitzer et al., *J. Biol. Chem.* 264: 20786-20795 (1989) which is incorporated herein by reference. The single-stranded DNA template for the mutagenesis reaction was prepared by cloning the full length wild-type human DHFR cDNA (from plasmid pHD80 obtained from Dr. G. Attardi, California Institute of Technology) in M13mp18. Site-directed mutagenesis was carried out using the Oligonucleotide-directed *In Vitro* Mutagenesis System by Amersham. Phosphorylation of the mutagenic oligonucleotide, annealing of the oligonucleotide with the DNA template, extension of the oligonucleotide with the Klenow fragment of DNA Polymerase I with α -thio-dCTP in place of dCTP, filtering of the reaction mixture to remove single-stranded DNA, nicking the non-mutant strand with the restriction enzyme *Nco*I (which cannot digest phosphorothioate DNA), removal of the nicked strand with exonuclease III, and repolymerization with *E. coli* DNA polymerase I were all carried out in accordance with the instructions of the manufacturer to produce S31 mutant DHFR.

Mutated cDNA was isolated from M13mp18 by digestion with *Nco*I and *Hind*III and ligated into a pKT7 vector fragment formed by digestion of pKT7HDR with *Nco*I and *Hind*III. The ligation mixture was transformed into *E. coli* BL21

S31 mutant DHFR was then used as the template for the introduction of a mutation at amino acid 22 using the same basic procedure. To introduce phenylalanine at this position, the complementary primers used were

5'-CCAGGGTTTGTCCCCGTT-3' and SEQ ID No. 1

3'-GGTCCCAAACAGGGGCAA-5', SEQ ID No. 3

the mutated regions being shown underlined. To introduce a tyrosine at amino acid 22, the complementary primers used were

5'-TGGCCAGGGTACGTCCCCGTTCTC-3' and SEQ ID No. 2

3'-ACCGGTCCCAATGCAGGGGCAAGAA-5'. SEQ ID No. 4

The PCR products were digested with *Nco*I/*Hind*III sites and subcloned into a pKT7 bacterial expression vector containing the same restriction sites. The resulting ligation mixtures were used to transform *E. Coli* BL21 to express the enzymes to be characterized.

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EXAMPLE 2

Gly31Phe22 and Gly31Tyr22 mutants of DHFR were prepared by a single-stranded DNA technique using the TRANSFORMER™ site-directed mutagenesis kit (Clontech). Two oligonucleotides were synthesized. The first was a mutation primer
5 containing the desired G31 mutation. This primer had the sequence

5' G CTC AGG AAT GAA GGC AGA TAT TTC CAG 3' SEQ ID No. 5

where the underlined portion is the mutation site. The second was a selection primer designed to destroy the unique PvuII restriction site and to create a unique KspI site on the pKT7 vector. The selection primer had the sequence

10 5' CGC GCG AGG CCG CGG CGG TAA AGC 3'. SEQ ID No. 6

These two primers were annealed to a single-stranded pKT7 vector containing either the Phe22 or the Tyr22 mutant DHFR cDNA and a second strand was synthesized which contained both desired mutations. The reaction mixture containing the two strands was digested with PvuII and then transformed into repair deficient BMH 71-18 mutS cells. The
15 transformed bacteria was used to prepare plasmid. To increase the transformation efficiency of the DNA containing the double mutants, plasmid preparations containing a mixture of single mutations and double mutations was linearized with PvuII. This reaction mixture was then transformed into *E. coli* DH5 α . The resulting colonies were screened using KspI digestion which only cuts plasmids containing the double mutant.

20

EXAMPLE 3

Enzyme expressed by the transformed *E. coli* was purified using an MTX-affinity column, followed by DEAE-Sephacel column chromatography. The purified enzymes were characterized to evaluate their kinetic parameters, and the results are summarized in
25 Table 2.

EXAMPLE 4

MFG Retroviral vectors containing mutant forms of DHFR can be constructed using the methods described by Riviere et al., *Proc. Nat'l Acad. Sci. (USA)* 92: 6733-6737
30 (1995) for human adenosine deaminase. To form the vector, 396 bp of 5' murine chromosomal DNA, an entire Moloney murine leukemia virus 5'LTR and adjacent sequence

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up until the NarI site at nt 1035, a sequence containing the viral 3' splice acceptor and spanning nt 5401-5780, having the A nucleotide of the NlaI site changed to C to create a NcoI site at the end of the this fragment, mutant human DHFR cDNA, MoMLV proviral sequences extending from the ClaI site at nt 7674 to the end of the 3' MoMLV LTR, and 695 bp of 3' murine chromosomal DNA are inserted into between the HindIII and EcoRI sites of plasmid pBR322.

EXAMPLE 5

After the viral constructs are made, GP-E86 cells, an ecotropic packaging line, and GP-AM12 cells, an amphotropic packaging line, are co-transfected with each vector using lipofection (DOTAP (Boehringer Mannheim, Germany)). Colonies are selected with G418. Surviving GP-E86 cells are collected, replated, and the supernatant is harvested, centrifuged at 3,000 rpm for 15 minutes to remove cell debris, and frozen at -80°C until use. G418 resistant GP-AM12 colonies are expanded, and supernatant subjected to titer measurement by infecting NIH 3T3 cells, using MTX as a selective agent. Briefly, 1×10^5 cells/60mm plate is exposed to appropriate dilutions of viral supernatant in the presence of 8 µg/ml of polybrene for 3 hours. Twenty-four hours later, transduced cells are exposed to 150 nM of MTX or 750 µg/ml of G418. Two weeks later, surviving colonies are counted and the titer calculated as cfu (colony-forming units)/ml of supernatant. The highest titer colonies for each vector are used as an amphotropic producer line. Also, the highest titer colonies of the amphotropic producer line are superinfected with ecotropic supernatants containing the same vector twice and if the titer increases, these resultant cells are used as producer lines.

EXAMPLE 6

To confirm the effectiveness of mutant DHFR in accordance with the invention to confer resistance to antifolate toxicity, *in vivo* experiments were conducted in mice using the Phe22/Ser31 (F/S) DHFR mutant. Bone marrow cells harvested from 5-fluorouracil treated donor mice were cocultured with virus producing AM12 cells producing SFG-F/S-Neo or SFG-Neo as a control for 24 hours. These cells were transplanted into both irradiated and nonirradiated recipients (2×10^6 and 2×10^7 cells per recipient). Bone marrow transplant recipients were challenged with a single dose of 300 mg/kg MTX during each of weeks 4 and 6 post transplant, and with a single dose of 600 mg/kg MTX during each of weeks 6 and 7

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post transplant. The recipients were monitored for survival, white blood cell counts, platelet counts, reticulocyte counts and drug resistant CFU-GM colonies. The observations indicated that recipient mice were protected from high dose MTX toxicity, while control animals could not tolerate high MTX doses. Further, it was observed that mDHFR cDNA transduced marrow cells are engrafted in both irradiated and nonirradiated recipients.

EXAMPLE 7

Bone marrow from primary transplant recipients was transplanted to secondary recipients, which were in turn tested for resistance to MTX toxicity using a CFU-GM assay. The results, which are summarized in Table 5, showed that protection against MTX toxicity can indeed be transferred, suggesting that an early progenitor cell population was transduced. PCR analysis demonstrated the presence of Neo^R cDNA in CFU-S colonies from secondary recipients.

TABLE 5			
Transduced with	Colonies (in the absence of drug)	Colonies in G418 (750 ug/ml G418)	Colonies in MTX (2X10 ⁻⁸ M MTX)
Normal Bone Marrow	92	0	0
SFG-Neo	88	26 (30%)	ND
SFG-F/S-Neo	104	47 (45%)	27 (26%)

SEQUENCE LISTING

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA

(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(v) FRAGMENT TYPE: internal
(ix) FEATURE: site-directed mutagenesis primer for human DHFR
(D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
CCAGGGTTTG TCCCCGTT 18

(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(v) FRAGMENT TYPE: internal
(ix) FEATURE: site-directed mutagenesis primer for human DHFR
(D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
TGGCCAGGGT ACGTCCCCGT TCTC 24

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: internal
(ix) FEATURE: site-directed mutagenesis primer for human DHFR
(D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
AACGGGGACA AACCTGG 18

(2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no

- 15 -

(iv) ANTI-SENSE: no
(v) FRAGMENT TYPE: internal
(ix) FEATURE: site-directed mutagenesis primer for human DHFR
(D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
AAGAACGGGG ACGTACCCTG GCCA 24

(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(v) FRAGMENT TYPE: internal
(ix) FEATURE: site-directed mutagenesis primer for human DHFR
(D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
GCTCAGGAAT GAAGGCAGAT ATTTCCAG 28

(2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: yes
(v) FRAGMENT TYPE: internal
(D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
CGCGCGAGGC CGCGGCGGTA AAGC 24